HU

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Rotkreuzstiftung Zentrallaboratorium Blutspendedienst

(B) STREET: Wankdorfstrasse 10

(C) CITY Bern 22

(E) COUNTRY: Switzerland

(F) POSTAL CODE (ZIP): CH-3000

(ii) TITLE OF INVENTION: Recombinant Fab-fragment with reactivity against Rhesus D antigens, DNA encoding them, complete antibodies comprising the Fab fragments and process for their preparation

(iii) NUMBER OF SEQUENCES: 64

(iv) COMPUTER READABLE RORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-QOS/MS-DOS

(D) SOFTWARE: PatentIn Release \$\\$1.0, Version \$\#1.30 (EPO)\$

(v) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/EP97X03253

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 96810421.6

(B) FILING DATE: 24-JUN-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO



PRECENTED DECISION

THOS DON

(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: N-terminal	
 (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B 	
(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-40	
 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number 	
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91105, 148198, 295342)	
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1375(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 48	
Gln Val Lys Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15	
TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 25 30	96
GCC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	

t

GCA GGT ATA TGG TTT GAT GGA AGT AAC AAA AAC TAT GCA GAC TCC GTG 192 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 50 55 60 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 70 65 75 80 CTG CAA CTG AAC AGC CTG AGA GAC GAG GAC ACG GCT GTG TAT TAT TGT 288 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 GCG AGA GAG CGA GCA CGT GGT ATT TCT AGG TTC TAT TAC TAC ATG 336 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Met 100 105 110 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC CCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Pro 115 120 125 (2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 20 25 30 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val

50	55	60		
Lys Gly Arg	Phe Thr Ile Se 70	r Arg Asp 75	Asn Ser Lys 80	s Asn Thr Leu Tyr
Leu Gln Leu 85			Hu Asp Thr A	Ala Val Tyr Tyr Cys
Ala Arg Glu 100	Arg Ala Ala A 105	rg Gly Ile	Ser Arg Phe 110	Tyr Tyr Tyr Met
Asp Val Trp	Gly Lys Gly T 120	hr Thr Va 12		r Pro
(2) INFORM	ATION FOR	SEQ ID N	IO: 3:	
(A) LE (B) TY (C) ST (D) TO	ENCE CHARA ENGTH: 318 b PE: nucleic ac TRANDEDNE OPOLOGY: lin	ase pairs cid SS: single near		
. ,	CULE TYPE: THETICAL: N		MKNA	
(iv) ANTI-	SENSE: NO			
(v) FRAG	MENT TYPE	: N-termir	ıal	
(A) OR (C) IN (D) DE (E) HA	INAL SOURCE RGANISM: HE DIVIDUAL IS EVELOPMEN PLOTYPE: d ELL TYPE: Pe	omo sapie SOLATE: TAL STA iploid	hyperimmun AGE: Adult	e Rhesus D donor
(A) LII	DIATE SOUR BRARY: cDN ONE: LD1-40	A library,	LD1	

(viii) POSITION IN GENOME:

(B) MAP POSITION: p11

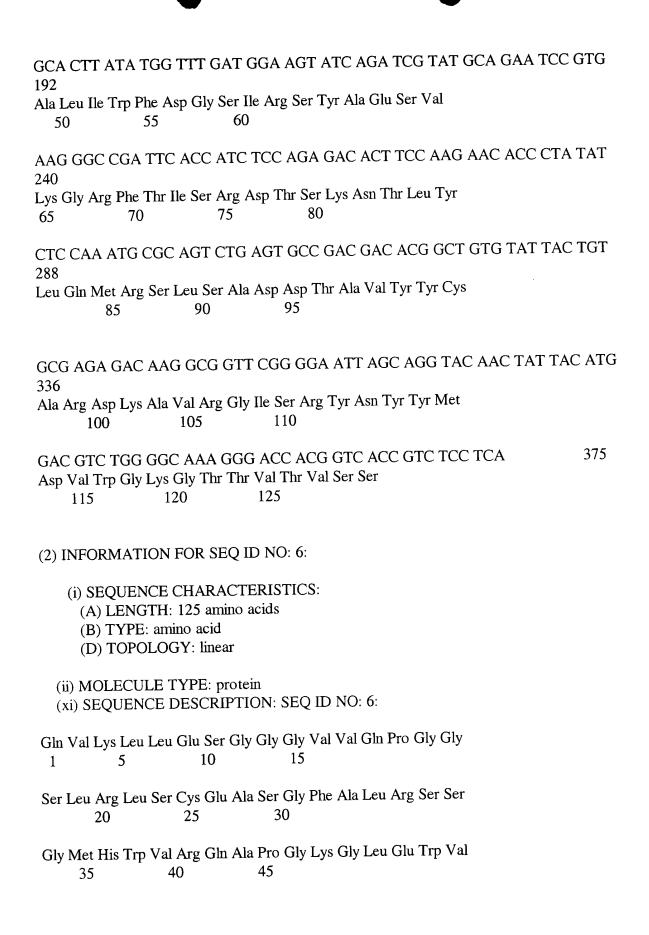
(A) CHROMOSOME/SEGMENT: Chromosome 2

(C) UNITS: Chromosome band number

(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..288) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGC GAC AGA 48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG TTG CTG ATC TAT GGT 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 35 GCG TCC ACT TTG CAA AGT GGC GTC CCA TCA AGG TTC AGT GGC AGT GGC Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60 TCT GGG GCA GTT TTC ACT CTC ACC ATC GCC AGT CTA CAA CCT GAA GAT Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 65 70 75 80 TTT GCA ACT TAC TGT CAA GAG AGT TAC AGT AAT CCT CTA ATC ACC 288 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 90 85 TTC GGC CAA GGG ACA CGA CTG GAG ACT AAA 318 Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly 45 40 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp 80 75 65 70 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr 90 95 85 Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-52 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5 1 TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC GCC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser 30 20 25 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 40



Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 70 75 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 85 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105 110 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-52 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: P 11

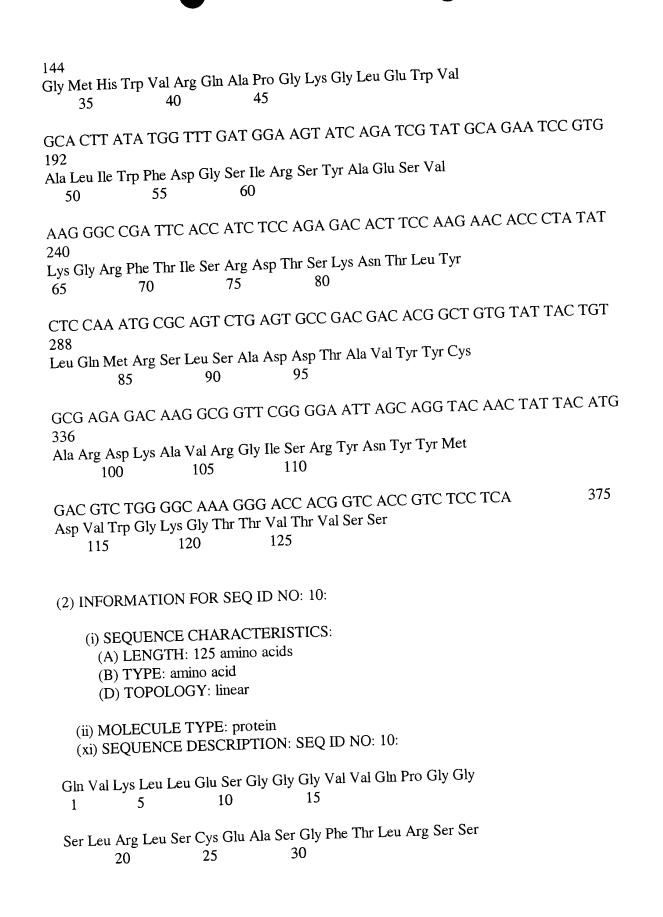
(C) UNITS: chromosome b.No
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259288)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT ATC CGC TAT TTA AAT
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn 20 25 30
TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT AGG CTC CTG ATC TAT GGT .44
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly 35 40 45
GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA 192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT AGT CTG CAA CCT GAA GAT
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80
TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC CGT ACC CCT CCA TTC ACT
288 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr 85 90 95

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 1 5 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly 40 45 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 80 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr 95 90 85 Phe Gly Pro Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-84 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 5 TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 25 30 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG



Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 60 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 11: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune rhsus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-84

(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGA GAC AGA 48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 15 10 5 GTC ACC ATC ACC TGC CGG GCA AGT CAG AGT ATC ATC AGG TAT TTG AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 TGG TAT CAG CAC AAA CCA GGA AAA GCC CCT AAA CTC CTC ATC TTT GCT 144 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala 45 40 35 GCA TCG AAT TTG CAA ACT GGG GTC CCA TCC AGG TTC AGT GGC AGT GGA Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGT GAC CTG CAG CCT GAG GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 80 75 TTC GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT AGG CCG TTC ACT TTT Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe

85 90 95

GGC CGG GGG ACC AGC CTG GAC ATC AAA Gly Arg Gly Thr Ser Leu Asp Ile Lys 100 105 315

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala 35 40 45

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp 65 70 75 80

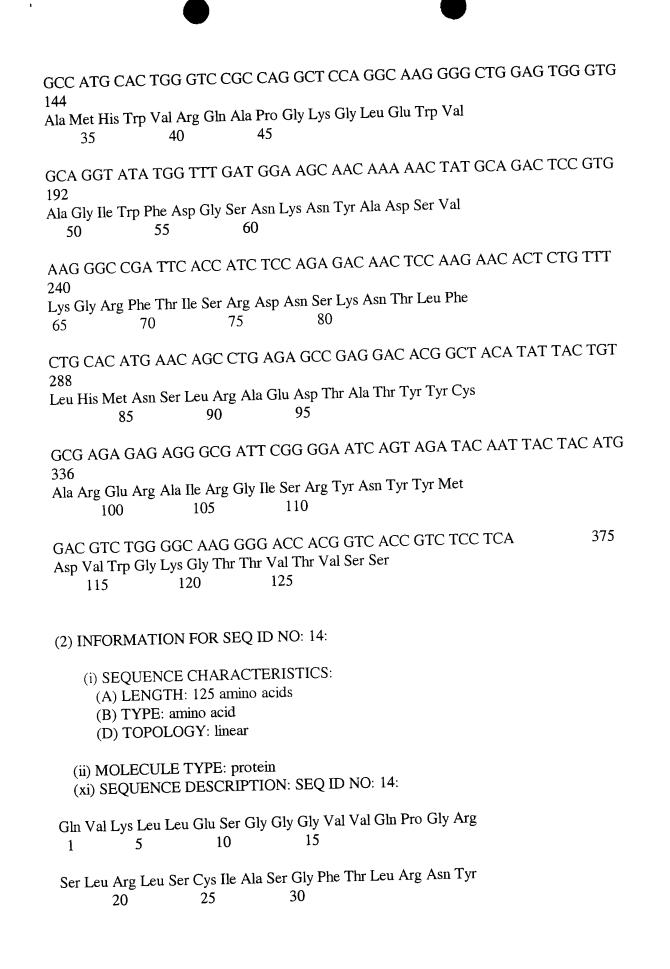
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe 85 90 95

Gly Arg Gly Thr Ser Leu Asp Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-110 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..348) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 15 10 5 1 TCC CTG AGA CTC TCC TGT ATA GCG TCT GGA TTC ACC CTC AGG AAT TAT 96 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr 30 25 20



Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val 60 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe 75 70 65 Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys 95 90 85 Ala Arg Glu Arg Ala Ile Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 15: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: Adult (E) HAPLOTYPE: Diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD1 (B) CLONE: LD1-110

(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: chromosome b.No (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT CGA AGC TCT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn 20 TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAA GTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala 40 35 GCA TCC AGT TTG CAA AGT GGG GTC CCA TCC AGG TTC AGT GGC AGA GGA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly 60 55 50 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAG CCT GAA GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 TTT GCG ACT TAT TAT TGT CAA CAG AGT TCC AGT TCC TCG TGG ACG TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe

85 90 95

GGC CAA GGG ACC AAG GTG GAA ATC AAA Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105 315

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

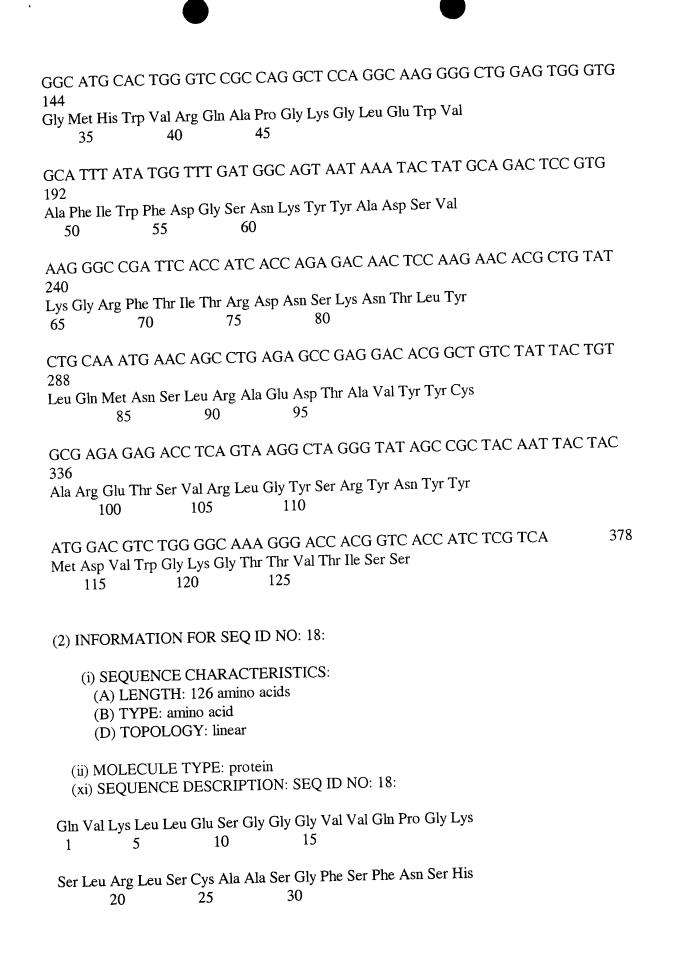
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Ser Trp Thr Phe 85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: N-terminal	
 (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B 	
(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-117	
 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number 	
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1378(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"	
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91105, 148198, 295345)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
CAG GTG AAA CTG CTC GAG TCA GGA GGC GTG GTC CAG CCT GGG AAG	
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Lys 1 5 10 15	
TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTC AGT TTC AAT AGC CAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His 20 25 30	96



Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 60 50 55 Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 90 95 85 Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr 110 105 100 Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Ile Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 19: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD1 (B) CLONE: LD1-117

 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1318(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259288)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA
48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGG AGC CAT TTG AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
GCA TCC AGT TTG CAA GGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA 192
Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80
TTT GCA ACT TAT TAC TGT CAA CAG AGT TAC AGG GCC CCT CAG TGG ACG 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr

85 90 95

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

318

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45

Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr 85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: N-terminal	
 (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B 	
(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA LIBRARY, LD2 (B) CLONE: LD2-1	
 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number 	
 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" 	
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91105, 148198, 295342)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48	
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	
TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 20 25 30	96

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG
144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG
192 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 50 55 60
AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 65 70 75 80
CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TGT 288
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 85 90 95
GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC CTG
Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 100 105 110
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125
(2) INFORMATION FOR SEQ ID NO: 22:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids
(B) TYPE: amino acid (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 75 70 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 85 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 23: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 333 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmund Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA LIBRARY, LD2 (B) CLONE: LD2-1 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 22 (B) MAP POSITION: q11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..333 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(61..99, 145..165, 262..294) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23: GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGA CAG AGG GTC Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val 15 10 5 1 ACC ATC TCT TGT TCT GGA AGC AAC TCC ATC CTT GGA AGT AAG TAT GTA 96 Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val 25 20 TAC TGG TAC CAG AAA CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr 45 40 35 AAG AAT GAT CAG CGG CCC TCA GGG GTC TCT GAC CGA TTC TCT GGC TCC Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 60 55 50 AAG TCT GGC ACC TCG GCC TCC CTG GCC ATC AGT GGG CTC CGG TCC GAG 240 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu 80 75 70 65

GAT GAG GCT GAC TAT TAC TGT GCA CCA TGG GAT GCC AAC CTG GGT GGC	
288 Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly 85 90 95	
CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 100 105 110	333
(2) INFORMATION FOR SEQ ID NO: 24:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 111 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:	
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val 1 5 10 15	
Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val 20 25 30	
Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr 35 40 45	
Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser 50 55 60	
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu 65 70 75 80	
Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly 85 90 95	
Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro 100 105 110	
(2) INFORMATION FOR SEQ ID NO: 25:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs	

.

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: homo sapiens (C) INDIVIDUAL ISOLATE: Hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA Library, LD2 (B) CLONE: LD2-4 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25: CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 1

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 60 50 55 AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 80 75 70 65 CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT 288 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 90 85 GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG 336 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 26: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 35 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 50 55 60 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 75 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 (2) INFORMATION FOR SEQ ID NO: 27: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 312 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid

(G) CELL TYPE:	Peripheral lym	phocyte B		
(vii) IMMEDIATE SO (A) LIBRARY: cI (B) CLONE: LD2	ONA library, L	D2		
(viii) POSITION IN GE (A) CHROMOSO (B) MAP POSITION (C) UNITS: Chron	ME/SEGMEN ON: p11		2	
(ix) FEATURE: (A) NAME/KEY: (B) LOCATION: (D) OTHER INFO	1312	product= "Immur	oglobulin, Fab"	
(ix) FEATURE: (A) NAME/KEY: (B) LOCATION:	CDR1, CDR2 join(6496, 14	2, CDR3 2162, 259282)		
(xi) SEQUENCE DE	SCRIPTION: S	SEQ ID NO: 27:		
GTG ATG ACC CAG	CT CCA TCC	C TCC CTG TCT	GCA TCT GTA G	GA GAC AGA
48 Val Met Thr Gln Ser Pro 1 5	o Ser Ser Leu 3	Ser Ala Ser Val (15	lly Asp Arg	
GTC ACC ATC ACT T	GC CGG ACA	A AGT CAG AC	C ATT AGC AGA	AAT TTA AAT
96 Val Thr Ile Thr Cys Arg 20 2	g Thr Ser Gln 7	Thr Ile Ser Arg A 0	sn Leu Asn	
TGG TAT CAG CAG	AAA CCA GG	G AAA GCC CC	T AAG CTC CTG	ATC TAT GCT
144 Trp Tyr Gln Gln Lys Pr 35 40	o Gly Lys Ala 45	Pro Lys Leu Leu	Ile Tyr Ala	
ACA TCC AGT TTG	CAA AGT GG	G GTC CCA TC	A AGG TTC AGT	GGC AGT GGA
Thr Ser Ser Leu Gln Se 50 55	er Gly Val Pro 60	Ser Arg Phe Ser	Gly Ser Gly	
TCT GGG ACA GAT 240	TTC ACT CT	C ACC ATC AA	T AGT CTA CAA (CCT GAA GAT

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp 75 65 TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCT TCG TTC GGC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly 95 90 85 312 CAA GGG ACC AAG GTG GAA ATC AAA Gln Gly Thr Lys Val Glu Ile Lys 100 (2) INFORMATION FOR SEQ ID NO: 28: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 104 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 5 1 Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn 30 20 25 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 40 45 35 Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 50 55 Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp 80 75 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly 90 95 85 Gln Gly Thr Lys Val Glu Ile Lys 100 (2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapiens

(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor

(D) DEVELOPMENTAL STAGE: adult

(E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library, LD2

(B) CLONE: LD2-4

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: chromosome 2

(B) MAP POSITION: p11

(C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..375

(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCG GGG GGG 48

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15		
Ser Leu A	G AGA CTO Arg Leu Ser 20	C TCC TGT Cys Val Al	GTA GC a Ser Gly 3	CG TCT GGA TTC ACC TTC AGG AGT TAT Phe Thr Phe Arg Ser Tyr	96
	G CAC TG	G GTC CG	C CAG G	CT CCA GGC AAG GGC CTG GAG TGG GTG	
144 Gly Met 35		Arg Gln Al 40	a Pro Gly 45	Lys Gly Leu Glu Trp Val	
GCT TT 192	T ATA TG	G TTT GAT	GGA AC	GT AAT AAA GGA TAT GTA GAC TCC GTG	
	Ile Trp Phe 55		Asn Lys (Gly Tyr Val Asp Ser Val	
AAG GO	GC CGA TI	C ACC AT	C TCC C	GA GAC AAT TCC AAG AAC ATG CTC TAT	
	Arg Phe Th	r Ile Ser Arg 75	g Asp Asn	Ser Lys Asn Met Leu Tyr 80	
CTG CA	AA ATG AA	AT AGC CT	G AGA G	GCC GAG GAC ACG GCT GTA TAT TAT TGT	
Leu Gln	Met Asn Se 85	er Leu Arg A 90	Ala Glu As 95	sp Thr Ala Val Tyr Tyr Cys	
	GA GAG A	AG GCG C	TT CGG (GGA ATC AGT AGA TAC AAC TAT TAC CTG	
-	Glu Lys Ala 100	a Leu Arg G 105	ly Ile Ser 110	Arg Tyr Asn Tyr Tyr Leu	
GAC G Asp Val	Trp Gly Ly	GC AAG GO es Gly Ala Ti 120	GG GCC A hr Val Thr 125	ACG GTC ACC GTC TCC TCA 375 r Val Ser Ser	
(2) INF	ORMATIO)	N FOR SEÇ) ID NO: 3	30:	
(1				CS:	
(ii) M (xi) S	IOLECULE SEQUENCE	E TYPE: pro E DESCRIP	tein TION: SE	Q ID NO: 30:	

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly 15 10 5 1 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr 75 70 65 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 110 105 100 Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 31: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 318 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDND library. LD2 (B) CLONE: LD2-5
 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number
 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1318 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259288)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA GGC GAC AGA 48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 1 5 10 15
1 5 10 15 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC GTT ACC AGG TCT TTA AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 20 25 30
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AGG CTC CTA ATC TTT GCT
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 35 40 45
GCG TCC ACT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA 192
Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACC CTC ACC ATC AGC AGT CTG CAA CCT GAG GAT 240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

TTT GGA ACT TAC TAC TGT CAA CAG AAT TAC AGG ACC CCT CAG TGG ACG Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 95 90 85 TTC GGC CAA GGG ACC AAG GTA GAA ATC AAA 318 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 32: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 106 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg 15 10 1 5 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala 40 45 35 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 75 80 70 65 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr 95 90 85 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-10 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..378 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 298..345) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC CTC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr 30 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 50 AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ATG GTC TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr 180 175 CTG CAA ATG AAC AGC CTG AGA GCC GAT GAC ACG GCT GTA TAT TAT TAT 288 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr 90 85 TGT GCG AGA GAG AAG GCG CTT CGG GGA ATC AGC AGA TAC AAC TAT TAC Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr 110 105 100 CTG GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCA 378 Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115

96

- (2) INFORMATION FOR SEQ ID NO: 34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5	1	10	15	
Ser Le	u Arg Let 20	Ser Cys 25	Val Ala	Ser Gly P 30	he Thr Leu Arg Ser Tyr
	et His Trp 35	Val Arg 40	Gln Ala	Pro Gly I 45	Lys Gly Leu Glu Trp Val
Ala Ph 50	ne Ile Trp	Phe Asp (Gly Ser A	Asn Lys C	lly Tyr Val Asp Ser Val
Lys G 65		e Thr Ile S	Ser Arg A	Asp Asn S	Ser Lys Asn Met Val Tyr 80
Leu G	Iln Met As 85		ı Arg Al 90	a Asp As _j 95	o Thr Ala Val Tyr Tyr Tyr
Cys A	la Arg Gl 100	u Lys Ala 10	Leu Arg 15	g Gly Ile S 110	Ser Arg Tyr Asn Tyr Tyr
	Asp Val Ti 115	p Gly Lys 120	s Gly Th	r Thr Val 125	Thr Val Ser Ser
(2) IN	NFORMA	TION FO	R SEQ I	D NO: 3	5:
(i)	(B) TYF (C) STR	NCE CHA IGTH: 33 PE: nucleio ANDEDI POLOGY	3 base page acid NESS: si	airs	3:
(ii)) MOLEC	ULE TY	PE: cDN	A to mR	NA
(iii) НҮРОТ	HETICA	L: NO		
(iv	v) ANTI-S	SENSE: N	10		
(v) FRAGN	MENT TY	/PE: N-t	erminal	
(v	(C) INI (D) DE (E) HA	GANISM	[: Homo L ISOL. ŒNTAL E: diploi	ATE: hyp . STAGE d	

s .

(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-10
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 22 (B) MAP POSITION: q11 (C) UNITS: Chromosome band number
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1333(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(61102, 148168, 265294)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
GTG GTG ACT CAG GAG CCC TCA CTG ACT GTG TCC CCA GGA GGG ACA GTC 48
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val 1 5 10 15
ACT CTC ACC TGT GCT TCC AGC ACT GGG GCA GTC ACC AGG GGT TAC TAT
96 Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr 20 25 30
CCA AAC TGG TTC CAG CAG AAG CCT GGA CAA GCA CCC AGG GCA CTG ATT
Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile 35 40 45
TAT AGT ACA AAC AAA AAA CAC TCC TGG ACC CCT GCC CGG TTC TCA GGC 192
Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly 50 55 60
TCC CTC CTT GGG GGC AAA GCT GCC CTG ACA CTG TCA GGT GTG CAG CCT 240
Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 65 70 75 80

GAA GAC GAG GCT GAA TAT TAC TGC CTG CTC TAC TAT GGT GGT GCT CAA	
288 Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln 85 90 95	
CTC GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA CGT CAG CCC Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro 100 105 110	333
(2) INFORMATION FOR SEQ ID NO: 36:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 111 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:	
Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val 1 5 10 15	
Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr 20 25 30	
Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile 35 40 45	
Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly 50 55 60	
Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro 65 70 75 80	
Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln 85 90 95	
Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro 100 105 110	
(2) INFORMATION FOR SEQ ID NO: 37:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs	

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-11 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342)
- CAG GTG AAA CTG CTC GAG TCG GGG GGA GGC GTG GTC CAG CCG GGG GGG
 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TCC CTG AGA CTC TCC TGT GAA GCG TCT GGA TTC ACC CTC AGA AGT TCT Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCT GGC AAG GGG CTG GAG TGG GTG 144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 GCA CTT ATA TGG TTT GAT GGA AGT ATC AGA TCG TAT GCA GAA TCC GTG Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 55 50 AAG GGC CGA TTC ACC ATC TCC AGA GAC ACT TCC AAG AAC ACC CTA TAT Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 80 75 70 65 CTC CAA ATG CGC AGT CTG AGT GCC GAC GAC ACG GCT GTG TAT TAC TGT 288 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 GCG AGA GAC AAG GCG GTT CGG GGA ATT AGC AGG TAC AAC TAT TAC ATG Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 105 100 GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 10 5 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val 60 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid

(G) CELL TYPE: lymphocvyte
(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-11
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number
 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
GTG TTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT ATA CGA GAC AGA
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT GGC AGT TAT TTA AAT
96 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn 20 25 30
TGG TAT CAG CAC AAA CCA GGG ACA GCC CCT AAA CTC CTG ATC TAT GCT
 144 Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
GTA TCC GCT TTG CAA AGT GGG GTC CCA TCG AGG TTC AGT GGC AGT AGA
 192 Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT CCC CCG TAC ACT TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe GGC CAG GGG ACC AAC CTG CAG ATC AAA Gly Gln Gly Thr Asn Leu Gln Ile Lys (2) INFORMATION FOR SEQ ID NO: 40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40: Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Arg Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Ser Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala Val Ser Ala Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe Gly Gln Gly Thr Asn Leu Gln Ile Lys (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-14 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5 1

TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT 96 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 25 20 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 60 55 50 AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT 240 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95 90 85 GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 120 125 115 (2) INFORMATION FOR SEQ ID NO: 42: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5		10		15	
Ser Le	u Arg Val 20	Ala Cys 25		a Ser C	lly Phe	Thr Phe Arg Asn Phe
	et His Trp 55	Val Arg 40	g Gln Al	a Pro (45	Gly Lys	s Gly Leu Glu Trp Val
Ala Ph 50	e Ile Trp	Phe Asp 55	Ala Ser	Asn L 60	ys Gly	Tyr Gly Asp Ser Val
Lys Gl		e Thr Va '0	al Ser Ar 75	g Asp	Asn Se 80	er Lys Asn Thr Leu Tyr
Leu G	ln Met As 85	sn Gly L	eu Arg A 90	Ala Glu	Asp T 95	'hr Ala Val Tyr Tyr Cys
Ala A	rg Glu Ly 100	s Ala Va 1	al Arg G 05	ly Ile S 1	er Arg 10	Tyr Asn Tyr Tyr Met
	al Trp Gl	y Lys Gl 120	ly Thr T	hr Val 125	Thr Va	al Ser Ser
(2) IN	IFORMA'	TION F	OR SEQ	ID N	O: 43:	
(i)	SEQUENT (A) LENT (B) TYP (C) STR (D) TOP	IGTH: 3 E: nucle ANDED	15 base ic acid ONESS:	pairs	rics:	
(ii)	MOLEC	ULE TY	PE: cD	NA to	mRNA	
(iii)	НҮРОТ	HETICA	L: NO			
(iv) ANTI-S	SENSE:	NO			
(v) FRAGN	MENT T	YPE: N	-termiı	ıal	
(v	(C) INI (D) DE (E) HA	GANISN	M: Homo AL ISOI MENTA PE: diplo	LATE: LL STA oid	hyperi	mmune Rhesus D donor dult

. .

(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-14
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1315(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTG GGA GAC AGA 48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
1 5 10 13 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AAC AAT TTA AAT
96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn 20 25 30
TGG TAT CAG CAG AAA CCA GGC AAA GCC CCT GAA CTC CTG ATC TAT GCT
144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala 35 40 45
GCA TCC AGT TTG CAA AGT GGG GTC CCT TCA AGG TTC CGT GGC AGT GGA
 192 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly 50 55 60
TCT GGG AGA GAT TTC ACT CTC ACC GTC ACC AGT CTG CAA CCT GAA GAT
 240 Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp 65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CTG TGG ACG TTC Phe Ala Thr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe 95 90 85 315 GGC CAA GGG ACC AAG GTG GAA ATC AAA Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 44: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala 40 35 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly 55 50 Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp 80 75 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe 95 90 85 Gly Gln Gly Thr Lys Val Glu Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 45: (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA llibrary (B) CLONE: LD2-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.43 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..375 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..342) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45: CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

15

10

5

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AGT TAT 96 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr 25 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 35 GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 60 55 50 AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ACG CTC TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 80 75 70 CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95 85 GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 110 105 100 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 46: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5	1	.0	15	
Ser Leu	Arg Let 20	Ser Cys 25	Val Ala	Ser Gly	Phe Thr Phe Arg Ser Tyr
Gly Me		val Arg 40	Gln Ala	Pro Gly 45	Lys Gly Leu Glu Trp Val
Ala Pho	e Ile Trp	Phe Asp (Gly Ser A	Asn Lys	Gly Tyr Val Asp Ser Val
Lys Gly		e Thr Ile S 70	Ser Arg A	Asp Asn	Ser Lys Asn Thr Leu Tyr 80
Leu Gl	n Met Ly 85		ı Arg Ala 90	a Glu As 95	p Thr Ala Val Tyr Tyr Cys
Ala Ar	g Glu Ly 100	s Ala Leu 10	Arg Gly	Ile Ser 110	Arg Tyr Asn Tyr Tyr Leu
	al Trp G 15	ly Lys Gly 120	Thr Thr	Val Th	r Val Ser Ser
(2) IN	FORMA	TION FO	R SEQ I	D NO: 4	47:
(i)	(A) LEN (B) TYN (C) STR	NCE CHANGTH: 31 PE: nucleic RANDEDI POLOGY	5 base page acid NESS: si	airs	CS:
(ii)	MOLEC	CULE TYI	PE: cDN	A to mF	RNA
(iii)	НҮРОТ	HETICA	L: NO		
(iv) ANTI-	SENSE: N	1O		
(v) FRAGI	MENT TY	/PE: N-t	erminal	
(vi	(A) OR (C) INI (D) DE (E) HA	NAL SOU GANISM DIVIDUA EVELOPM PLOTYP ELL TYPE	(: Homo L ISOL. IENTAL E: diploi	ATE: hy LSTAGI .d	

•

(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-17
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1315(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
GTG ATG ACC CAG TCT CCA TTC TCC CTG TCT GCA TCT GTA GGA GAC AGA
48 Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg
1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AAC ATT AGG AGT TTT TTA AGT
96 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 20 25 30
TGG TAT CAG CAG AAA CCA GGG ACA GCC CCT AAG CTC CTG ATC TAT GCT
144 Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
GCA TCC AGG TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGG
 192 Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC ACT CTG CAA CCT GAA GAT
 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80

TTT GCG ACT TAC TAC TGT CAA CAG AGT TAC AGT GCC CCT TGG ACG TTC
288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 85 90 95
GGC CAA GGG ACC AAG CTG GAA ATC AAA Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105
(2) INFORMATION FOR SEQ ID NO: 48:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 105 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser 20 25 30
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp 65 70 75 80
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe 85 90 95
Gly Gln Gly Thr Lys Leu Glu Ile Lys 100 105
(2) INFORMATION FOR SEQ ID NO: 49:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 375 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library LD2
 - (B) CLONE: LD2-20
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..375
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION:join(91..105, 148..198, 295..342)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG 48

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15

10

TCC CTG AGA CTC TCC TGT GTA GCG TCT GGA TTC ACC TCC AGG AGT TAT Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr 30 20 25 GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 55 60 50 GCT TTT ATA TGG TTT GAT GGA AGT AAT AAA GGA TAT GTA GAC TCC GTG Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val 80 75 70 65 AAG GGC CGA TTC ACC ATC TCC CGA GAC AAT TCC AAG AAC ACG CTC TAT 240 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 90 85 CTG CAA ATG AAG AGC CTG AGA GCC GAG GAC ACG GCT GTA TAT TAT TGT 288 Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 110 105 100 GCG AGA GAG AAG GCG CTT CGG GGA ATC AGT AGA TAC AAC TAT TAC CTG Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu 215 210 205 GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA 375 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 115 120 (2) INFORMATION FOR SEQ ID NO: 50: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5		10	1:	5		
Ser Lei	ı Arg Leu 20	Ser Cys 25	Val Ala	Ser Gly 30	y Phe Thr	Ser Arg Ser T	yr
	et His Trp 5	Val Arg 40	Gln Ala	Pro Gl 45	y Lys Gly	Leu Glu Trp V	√al
Ala Ph 50	e Ile Trp	Phe Asp 55	Gly Ser A	Asn Ly)	s Gly Tyr	Val Asp Ser V	al
Lys Gl 65		e Thr Ile 0	Ser Arg 75	Asp As	sn Ser Lys 80	Asn Thr Leu	Гуг
Leu G	ln Met Ly 85	s Ser Le	u Arg Al 90	a Glu A	Asp Thr A	la Val Tyr Tyr	Cys
Ala A	rg Glu Ly 100	s Ala Lei 10	u Arg Gly 05	y Ile Se 11	r Arg Tyr 0	Asn Tyr Tyr I	æu.
	al Trp Gl 15	y Lys Gl 120	y Thr Th	r Val T 125	hr Val Se	r Ser	
(2) IN	IFORMA'	TION FO	OR SEQ	ID NO	: 51:		
(i)	SEQUEN (A) LEN (B) TYP (C) STR (D) TOP	GTH: 31 E: nuclei ANDED	15 base p ic acid NESS: s	airs	CS:		
(ii)	MOLEC	ULE TY	PE: cDN	IA to m	nRNA		
(iii)	НҮРОТ	HETICA	L: NO				
(iv) ANTI-S	ENSE: 1	O				
(v) FRAGN	MENT T	YPE: N-t	ermina	1		
(v	(C) INI (D) DE (E) HA	GANISM DIVIDUA VELOPM PLOTYH	1: Homo AL ISOL MENTAI PE: diplo:	ATE: h L STA(id	s nyperimmu GE: adult mphocyte	une Rhesus D d	lonor

,

(vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD2 (B) CLONE: LD2-20
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1315(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:
GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA 48 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT AGC AGC TAT TTA AAT 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
TGG TAT CAG CAG AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT 144 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 35 40 45
GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGT GGC AGT GGA 192 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 50 55 60
TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT 240 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 65 70 75 80

TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CGA TTC ACT TTC Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe 95 90 85 315 GGC CCT GGG ACC AAA GTG GAT ATC AAA Gly Pro Gly Thr Lys Val Asp Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 52: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 10 15 5 1 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn 30 25 20 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 60 55 50 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp 80 75 70 65 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe 95 90 85 Gly Pro Gly Thr Lys Val Asp Ile Lys 105 100 (2) INFORMATION FOR SEQ ID NO: 53: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 384 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-6-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 14 (B) MAP POSITION: q32.3 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..384 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(91..105, 148..198, 295..351) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:
- CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG 48

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

5

10

15



TCC CTG AGA CTT TCC TGT GCA GCG TCT GGA TTT ACC TTC AGT AGC TAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20

25

30

GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

GCA GAT ATA TGG TTT GAT GGA GGT AAT AAA CAT TAT GCA GAC TTC GTG 192

Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 50 55 60

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT $240\,$

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 65 70 75 80

CTA CAA ATG AAC AGC CTG AGA GTC GAG GAC ACG GCT GTG TAT TAC TGT 288

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

GCG AGG GAT TAC TAT AGC GTT ACT AAG AAA CTC AGA CTC CAC TAC TAC 336

Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 100 105 110

TAC TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA 384

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 220 225 230

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 10 5 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 30 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val 60 55 50 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr 75 70 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys 95 90 85 Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr 110 105 100 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult

(E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 (B) CLONE: LD1-6-17 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA ACC 96 Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr 30 25 20 TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala 45 40 35 GCA TCC AAT TTA CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly 55 60 50 TCT GGC ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp TTT GCA ACT TAT TAC TGT CTA CAA GAT AAC AAT TTC CCG TAC ACT TTT Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe GGC CAG GGG ACC AAG CTG GAG ATC AAA Gly Gln Gly Thr Lys Leu Glu Ile Lys (2) INFORMATION FOR SEQ ID NO: 56: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys (2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor

(D) DEVELOPMENTAL STAGE: adult

(E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library, LD1 and LD2

(B) CLONE: LD1/2-6-3

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: chromosome 14

(B) MAP POSITION: q32.3

(C) UNITS: Chromosome band number

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..375

(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"

(ix) FEATURE:

(A) NAME/KEY: CDR1, CDR2, CDR3

(B) LOCATION:join(91..105, 148..198, 295..342)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly

1	5	10	15			
Ser Leu A	G AGA GTC Arg Val Ala (20	CGCC TGT G Cys Val Ala Se 25	TA GCG Ter Gly Phe 7	CT GGA TTC ACC TTC AG Thr Phe Arg Asn Phe	GG AAT TTT	96
	G CAC TGO	G GTC CGC C	CAG GCT C	CA GGC AAG GGG CTG	GAG TGG GTG	
144 Gly Met 35	His Trp Val 4			Gly Leu Glu Trp Val		
GCT TT 192	T ATT TGG	TTT GAT G	CA AGT A	AT AAA GGA TAT GGA G	SAC TCC GTT	
Ala Phe 3	Ile Trp Phe A	Asp Ala Ser As 60	n Lys Gly T	Syr Gly Asp Ser Val		
	GC CGA TT	C ACC GTC T	CC AGA (GAC AAT TCC AAG AAC	ACG CTC TAT	
240 Lys Gly 65	Arg Phe Thr 70	Val Ser Arg A 75	Asp Asn Ser 80	Lys Asn Thr Leu Tyr		
288				GAA GAC ACG GCT GTA	TAT TAT TGT	
Leu Gln	Met Asn Gly 85	y Leu Arg Ala 90	Glu Asp Th 95	ır Ala Val Tyr Tyr Cys		
GCG A0	GA GAG AA	AG GCG GTT	CGG GGA	ATT AGT AGA TAC AAC	C TAC TAC ATG	
Ala Arg	Glu Lys Ala 100	Val Arg Gly I 105	le Ser Arg ' 110	Гуг Asn Туг Туг Met		
GAC G Asp Val	Trp Gly Lys	s Gly Thr Thr `	ACC ACG Val Thr Val 125	GTC ACC GTC TCC TCA Ser Ser	375	
(2) INF	ORMATION	N FOR SEQ II	NO: 58:			
()						
(ii) M (xi) S	OLECULE SEQUENCE	TYPE: protein	n DN: SEQ II) NO: 58:		

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 30 25 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 60 55 50 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 95 90 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 59: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (C) INDIVIDUAL ISOLATE: hyperimmune Rhesus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid

(G) CELL TYPE: Peripheral lymphocyte B (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA library, LD1 and LD2 (B) CLONE: LD1/2-6-3 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..315 (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab" (ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(64..96, 142..162, 259..285) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59: GTG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 15 10 5 1 GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 30 25 20 TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT ACT Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr 45 35 GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 60 50 55 TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTG CAA CCT GAA GAT

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC ACT ACC CCG TAC ACT TTT Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe GGC CAG GGG ACC AAG CTG CAG ATC AAA Gly Gln Gly Thr Lys Leu Gln Ile Lys (2) INFORMATION FOR SEQ ID NO: 60: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60: Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Gln Ile Lys

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (C) INDIVIDUAL ISOLATE: hyperimmune Rhesud D donor
 - (D) DEVELOPMENTAL STAGE: adult
 - (E) HAPLOTYPE: diploid
 - (G) CELL TYPE: Peripheral lymphocyte B
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA library, LD1 and LD2
 - (B) CLONE: LD1/2-2-33
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: chromosome 14
 - (B) MAP POSITION: q32.3
 - (C) UNITS: Chromosome band number
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..375
 - (D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDR1, CDR2, CDR3
 - (B) LOCATION:join(91..105, 148..198, 295..342)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCG GGG GGG

48 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 1 5 10 15	
TCC CTG AGA GTC GCC TGT GTA GCG TCT GGA TTC ACC TTC AGG AAT TTT Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 20 25 30	96
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	
144 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45	
GCT TTT ATT TGG TTT GAT GCA AGT AAT AAA GGA TAT GGA GAC TCC GTT	
192 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 50 55 60	
AAG GGC CGA TTC ACC GTC TCC AGA GAC AAT TCC AAG AAC ACG CTC TAT	
 240 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80 	
CTG CAA ATG AAC GGC CTG AGA GCC GAA GAC ACG GCT GTA TAT TAT TGT	
288 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95	
GCG AGA GAG AAG GCG GTT CGG GGA ATT AGT AGA TAC AAC TAC TAC ATG	
336 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 100 105 110	
GAC GTC TGG GGC AAG GGG ACC ACG GTC ACC GTC TCC TCA Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120 125	
(2) INFORMATION FOR SEQ ID NO: 62:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 125 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62: Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly 15 10 5 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe 30 25 20 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 45 40 35 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val 55 50 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 75 70 65 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 90 85 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met 110 105 100 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 125 120 115 (2) INFORMATION FOR SEQ ID NO: 63: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 315 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (v) FRAGMENT TYPE: N-terminal (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens

 (C) INDIVIDUAL ISOLATE: hyperimmune Resus D donor (D) DEVELOPMENTAL STAGE: adult (E) HAPLOTYPE: diploid (G) CELL TYPE: Peripheral lymphocyte B
(vii) IMMEDIATE SOURCE:(A) LIBRARY: cDNA library, LD1 and LD2(B) CLONE: LD1/2-6-33
 (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: chromosome 2 (B) MAP POSITION: p11 (C) UNITS: Chromosome band number
(ix) FEATURE:(A) NAME/KEY: CDS(B) LOCATION:1315(D) OTHER INFORMATION:/product= "Immunoglobulin, Fab"
(ix) FEATURE: (A) NAME/KEY: CDR1, CDR2, CDR3 (B) LOCATION:join(6496, 142162, 259285)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:
GTG ATG ACC CAG TCT CCA TCC TTC CTG TCT GCA TCT GTA GGA GAC AGA
Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg 1 5 10 15
GTC ACC ATC ACT TGC CGG GCA AGT CAG AGC ATT ATC AGA TAT TTA AAT 96
Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn 20 25 30
TGG TAT CAG CAC AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC CAT GCT 144
Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala 35 40 45
GCA TCC AGT TTG CAA AGT GGG GTC CCG TCA AGG TTC AGT GGC AGT GTA
192 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val 50 55 60

